

Appl. No. : 09/539,032
Filed : March 30, 2000

REMARKS

Claim 1 has been amended. Thus, claims 1-4 and 6-9 remain pending in the present application. Support for the amendments to claim 1 may be found in the specification at page 10, next to last paragraph; pages 5-7; pages 13-15; page 2, lines 4-6; and in original claim 11. Thus, no new matter has been added. Reconsideration and withdrawal of the present rejection in view of the comments presented herein are respectfully requested.

Rejection under 35 U.S.C. § 101

Claims 1-4 and 6-9 were rejected under 35 U.S.C. § 101 as allegedly being directed to non-statutory subject matter. Specifically, the Examiner alleged that the present claims only provide steps of *in silico* information manipulation, and do not result in a physical transformation of matter such that a tangible result is obtained. In addition, the Examiner alleges that the method steps are “not limited to any **particular apparatus or machinery.**” (Emphasis original).

Claim 1 as amended recites that: (1) steps i), iii), iv) and v) are performed using particular software programs; (2) steps i) and iii) are performed using one or more computer processors; and (3) conserved peptide motifs useful as drug targets for use in a host organism are obtained as a result of the recited method steps. Thus, the claims as amended clearly result in a physical transformation of matter such that a tangible result (conserved peptide motifs useful as drug targets for use in a host organism) is obtained as a result of the information manipulation recited in the claimed method. In addition, the method steps are now tied to particular software programs and machinery. Thus, the pending claims are now clearly directed to statutory subject matter.

In view of the comments presented above, Applicants respectfully request reconsideration and withdrawal of the rejection under 35 U.S.C. § 101.

Rejection under 35 U.S.C. § 112, second paragraph

Claims 1-4 and 6-9 were rejected under 35 U.S.C. § 112, second paragraph as allegedly being indefinite. The Examiner notes that while claim 1 recites “wherein all of said steps are performed on said computer,” that no “computer” was previously recited in the claim. Claim 1 as amended recites “a computer” rather than “said computer.”

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In view of the comments presented above, Applicants respectfully request reconsideration and withdrawal of the rejection under 35 U.S.C. § 112, second paragraph.

Rejection Under 35 U.S.C. §102(b)

The rejection of Claims 1-4 and 6-9 under 35 U.S.C. §102(b) as allegedly being anticipated by Bruccoleri et al (*Nucl. Acids Res.* 26:4482-2286, 1998) was again maintained.

The Examiner contends that Bruccoleri et al. teach all of the limitations of Claim 1 (generation of overlapping sequence alignments from pathogenic organisms; homolog matching; target sequence alignment for all sequences; alignment of just matching gene product against the corresponding gene product in the target; and exclusion criteria). Applicants respectfully disagree with the Examiner's position regarding this reference for the reasons set forth in their previous responses.

Bruccoleri et al disclose a computational tool to determine concordance of putative gene products. The method of Bruccoleri et al. aligns sets of selected proteins using FASTA and CLUSTALW programs to identify conserved regions across various proteins, BLOSSOM and PAM scoring matrices to identify approximate matches of conserved protein regions. These scoring methods identify non-exact matches. In contrast, the present claims recite exactly matched common peptide sequences. Thus, the present invention is entirely different from the method of concordance analysis of microbial genomes used by Bruccoleri et al.

One of ordinary skill in the art will realize that comparison of proteins by "Global alignment" which is used by FASTA is different than comparison of proteins using peptide blocks as recited in the present claims.

With regard to claim 2, Bruccoleri et al. teaches aligned sequences of length 4 where as the present invention refers to matched common peptides of length 4 or more. One significant unexpected advantage of the presently claimed invention is that the matched common peptide can come from any region of the protein to be compared as illustrated by the following example:

Seq 1: XXXXPQRSABCDYYXXXXYY
Seq 2: XXXXXYYYYCDABPQRSYY

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In this example, the peptide <PQRS>, although not aligned, can be identified by the presently claimed invention as matched common peptides which differentiate the presently claimed method from Bruccoli et al.

With regard to claim 3, *M. tuberculosis* is a known pathogen and selection of the same by Bruccoli et al. does not teach the method of identification of common peptides from a group of pathogenic organisms as potential drug targets.

With regard to claims 4 and 6, identification of DNA gyrase does not explicitly teach the importance of the peptide "VRKRPGMYIG" as a potential drug binding region. The present invention highlights the method of identification of such crucial "hot spots" that forms the basis of drug targeting. In present claim 4, there is no similarity in the methods of identification of conserved targets described in the cited reference and the present claims. SEQ ID NO: 67 is a stretch of specific conserved peptide sequence from DNA gyrase. Although Bruccoli et al. predicts a conserved region of DNA gyrase, no sequence is disclosed which matches SEQ ID NO. 67. The mere mention of DNA gyrase by the cited reference does not inherently disclose SEQ ID NO. 67 as a subunit of DNA gyrase which itself is a protein of MW 92 KDa, while SEQ ID NO. 67 is a small conserved peptide of 10 amino acid residues identified by the presently claimed method.

With regard to claim 8, Bruccoli et al. does not teach locating matched peptide sequences in the selected protein sequences. Identification of the matched common peptides, locating these in the protein sequence, and labeling them with an ID is an integral part of the software "PEPLIMP" & "PEPEXTRACT" used in the presently claimed invention.

Nonetheless, in order to expedite prosecution of the application, several steps of claim 1 have been amended to recite particular software programs which are neither disclosed nor suggested by Bruccoli et al. If the Office Action at page 7, last two paragraphs, the Examiner notes that although Applicant's assertion that "the software used to perform the protocols disclosed in the present application and the cited reference is different," "as there is no software recited in the instant claims, the prior art of record performs the same method and therefore anticipates each of said claims." Since software is recited in the present claims, the cited reference clearly does not perform the method recited in the present claim, and thus does not anticipate, or render obvious, the present claims.

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In view of the comments presented above, Applicants respectfully request reconsideration and withdrawal of the rejection under 35 U.S.C. §102(b).

CONCLUSION

Applicants submit that all claims are in condition for allowance. If any issues remain that could be resolved by telephone, the Examiner is cordially invited to contact the undersigned at the telephone number provided below. Please charge any additional fees, including any fees for additional extension of time, or credit overpayment to Deposit Account No. 11-1410.

Respectfully submitted,

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